

SEQUENCE LISTING

<110> Cotttingham, Ian R.  
McCreath, Graham E.

<120> Fusion Proteins Incorporating Lysozyme

<130> 0623.0730002/EKS/BJD

<140> US (to be assigned)  
<141> 2001-12-21

<150> US (to be assigned)  
<151> 2001-12-21

<150> PCT/GB00/02459  
<151> 2000-06-23

<150> GB 9914733.2  
<151> 1999-06-23

<150> US 60/147,819  
<151> 1999-08-10

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Linker

<400> 1

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
1 5 10 15

<210> 2

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recognition  
site for enzymatic cleavage

<400> 2

Ile Glu Gly Arg  
1

<210> 3

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recognition

site for enzymatic cleavage



acatttagt aataaacgc catatgccc ttatgcact taaaagtgt taacatttt 6600  
ccatagtgc ttcttcatg cttttttt ttttttttgc gagaggatc 6660  
ttgtgggtt ttgttgtt tattttgaga cagggttc tgcccccgg ctgtatcg 6720  
tggcaccate acagctca ctggatcc tgcataccc accacagcc cccaatgtc 6780  
ttggactaca ggtgtgcacc accatgcgt gaaatattt gaaatattttt 6840  
attctgtgtt gccaggctg gtcttgaact cttgagttca agcaatcttc 6900  
ctccatggc tgcgtggattt acaggcgta gcaactgttcc tggtctatgc 6960  
ttaatgtat taggaacatg atgatattcc atttcaataat ttttttttttgc 7020  
aaaatacagt tcctgtggaa ttatattgtt aaataaaaaa ttaacttaag gattttttt 7080  
tttgagtgta aaaaaatattt ttaactgtt ctttttttttgc 7140  
cagtgtcaaa aattatgcg aatttgcgt aatttttttttgc 7200  
aaatccccca taaaagacat taatcttgc ttttttttttgc 7260  
attataataat aattttgtt ctttttttttgc 7320  
accatataatc ttactacccca gagggtttt accatggta aatttgcgttcc 7380  
cagaatgtat atcaatcatg ttttttttttgc 7440  
atcaaaaaatc gtttttttttgc 7500  
ttcaatattt ctttttttttgc 7560  
taatgtatcc ttgtccattt ctttttttttgc 7620  
aaaagaatgt aatggatgtt aatattgtt aatatttttttgc 7680  
tatttgcacat ttgggtttt ctttttttttgc 7740  
atatactttt ggggttttttgc 7800  
agtttttttttgc 7860  
ttgttataatc ctttttttttgc 7920  
catgtctaat gggagaaaaa gaagagatgt ttttttttttgc 7980  
tagaaaaataa ttttttttttgc 8040  
aatttttttttgc 8100  
tgcataatcatc ttgggtttt ctttttttttgc 8160  
gcatttagacat ttgggtttt ctttttttttgc 8220  
tttttttttgc 8280  
tatataatcatc ttgggtttt ctttttttttgc 8340  
agcttttttgc 8400  
atgtatccatc ttgggtttt ctttttttttgc 8460  
aaagatgttcc acactttatc ttgggtttt ctttttttttgc 8520  
atgttggccc gggccatgtt ccacccctgtt ttttttttttgc 8580  
atggatcaccc ttgggtttt ctttttttttgc 8640  
ccactaaaaaa ttttttttttgc 8700  
tttttttttgc 8760  
tttttttttgc 8820  
tttttttttgc 8880  
tttttttttgc 8940  
tttttttttgc 9000  
tttttttttgc 9060  
tttttttttgc 9120  
tttttttttgc 9180  
tttttttttgc 9240  
tttttttttgc 9300  
tttttttttgc 9360  
tttttttttgc 9420  
tttttttttgc 9480  
tttttttttgc 9540  
tttttttttgc 9600  
tttttttttgc 9660  
tttttttttgc 9720  
tttttttttgc 9780  
tttttttttgc 9840  
tttttttttgc 9900  
tttttttttgc 9960  
tttttttttgc 10020  
tttttttttgc 10080  
tttttttttgc 10140  
tttttttttgc 10200  
tttttttttgc 10260  
tttttttttgc 10320

ttctgcacac	acagaacgga	gatccaaacca	gttcatccta	aaggagatca	gtctgggttg	10380
ttctatgggg	ggactgtgt	tggaaatcgaa	actccaaatgc	tttggccccc	ttgtatggaa	10440
agtctggact	ttttaaaaaa	ccctgtatgt	ggaaagattt	ggggggccgg	ggggaaagggg	10500
acagcaggagg	atagatgtgt	tggatggcat	cacaacacaa	atggacatgg	gtttgggttg	10560
actccaggag	tttgtgttgg	acaggggcgc	cttcggctgt	ggggggccaaa	ggggccaaaa	10620
gactgatgt	ctgaaatgtag	ctgaaatgtaa	tggaaatgtag	gtatcacaga	aagtggggat	10680
tttttagata	ataaaatgtat	acacataaaca	tagtgtatcat	tcatatttt	atgcataact	10740
gaatgttcag	tcaatctatgtc	gtatctgact	tcgttgcata	ttccggccatgt	ttttccatctc	10800
ttcttcgttc	cacaatgtttcc	tccggcggaa	aatactggag	ttggggtagcc	ttttccatctc	10860
cagggggttc	ttccggacccaa	ggggatgttac	cggtatctcc	tgatattgtca	gggtggatct	10920
tttacactgt	ggcaccagggg	aaaggccctgt	tactcttctat	ttccccactta	attaccaaag	10980
ctgtccatgg	aaaaaaacccgg	tgtggctctgt	agcttcccccgg	cctggcagagg	gttgggggggg	11040
tagactgt	cctggggaaaca	ccccccctgt	tcaggacttgc	ggggccacatgt	gaccacatgt	11100
cttgcagacaa	ggccgggttage	tctgtcttc	aagggttctt	atctttaaaaa	aaaatcgagg	11160
tctattttgt	gacttcgtgt	tcgtttatgtc	ttttttatccaa	gttgcgtatgg	cagccctctc	11220
cccagggttc	gggggtttcca	ggggagccgc	tttccatctat	gttgcgtatgg	acactcgggg	11280
gttggcccccgc	cttcgggttgg	cttcacatgt	ttccatctgtc	ttttttatccaa	aaacgacacca	11340
atgtacttttt	aggagacaaatc	agacacccac	ttttttatccaa	ttttttatccaa	actgtatgt	11400
cttttttttttt	ctaaagacacat	acatgttgc	aaagggtttttt	ttttttatccaa	gtttaatggc	11460
ctacttgcgc	ctaaagagggg	aaacatgttc	ttttttatccaa	ttttttatccaa	acttgcgtgc	11520
atcccgaggcc	acttagtatt	atctggccgc	ttttttatccaa	ttttttatccaa	ttttttatccaa	11580
aaaaaaatccgt	tggggaaatgtt	catccatgtt	ttttttatccaa	ttttttatccaa	ttttttatccaa	11640
tcttttttttcc	ttttttatgtt	atgtatgtat	ttttttatccaa	ttttttatccaa	ttttttatccaa	11700
ttttttttttgt	gtctgggtttgt	ttttttatccaa	ttttttatccaa	ttttttatccaa	ttttttatccaa	11760
ctatgtttttt	tttatcacatgt	ttttttatccaa	ttttttatccaa	ttttttatccaa	ttttttatccaa	11820
tttttttttttt	ttttttatccaa	ttttttatccaa	ttttttatccaa	ttttttatccaa	ttttttatccaa	11880
aaggccatccc	ttttttatccaa	ttttttatccaa	ttttttatccaa	ttttttatccaa	ttttttatccaa	11940
atgggggggg	ttttttatccaa	ttttttatccaa	ttttttatccaa	ttttttatccaa	ttttttatccaa	12000
gaggggactgt	ttttttatccaa	ttttttatccaa	ttttttatccaa	ttttttatccaa	ttttttatccaa	12060
c						12061

<210> 5  
<211> 7

<212> PRT  
<213> Artificial Sequence

≤220>

<223> Description of Artificial Sequence: Cleavage site  
recognised by enterokinase

<400> 5  
Phe Pro Thr Asp Asp Asp Lys  
1 5

<210> 6  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Linker arm

<400> 6  
 Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala  
           1             5             10             15

Ser

<210> 7

<211> 5  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Enterokinase cleavage site

<400> 7  
Asp Asp Asp Asp Lys  
1 5

<210> 8  
<211> 15  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<221> CDS  
<222> (1)..(15)  
  
<220>  
<223> Description of Artificial Sequence: Normal lysozyme C-terminal

<400> 8  
ggt tgt gga gtg taa  
Gly Cys Gly Val  
1 5

15

<210> 9  
<211> 4  
<212> PRT  
<213> Artificial Sequence  
<223> Description of Artificial Sequence: Normal lysozyme C-terminal  
  
<400> 9  
Gly Cys Gly Val  
1

<210> 10  
<211> 167  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<221> CDS  
<222> (1)..(162)  
  
<220>  
<223> Description of Artificial Sequence: C terminal extension

<400> 10  
ctc gag gga gga gga agc gga ggc ggc ggc agc gga ggc gga gga 48  
Leu Glu Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly  
1 5 10 15

agc gct agc atg tgc tcc aac ctg tcc acc tgc gtg ctg ggc aag ctg 96  
Ser Ala Ser Met Cys Ser Asn Leu Ser Thr Cys Val Leu Gly Lys Leu  
20 25 30

agc cag gag ctg cac aag ctg cag acc tac cct agg acc aac acc ggc 144  
Ser Gln Glu Leu His Lys Leu Gln Thr Tyr Pro Arg Thr Asn Thr Gly  
35 40 45

agc ggc acc cct gga taa tcgat 167  
Ser Gly Thr Pro Gly  
50

<210> 11  
<211> 53  
<212> PRT  
<213> Artificial Sequence  
<223> Description of Artificial Sequence: C terminal extension

<400> 11  
Leu Glu Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly 1 5 10 15  
Ser Ala Ser Met Cys Ser Asn Leu Ser Thr Cys Val Leu Gly Lys Leu  
20 25 30  
Ser Gln Glu Leu His Lys Leu Gln Thr Tyr Pro Arg Thr Asn Thr Gly  
35 40 45  
Ser Gly Thr Pro Gly  
50